

Fig. 1

Fig. 2

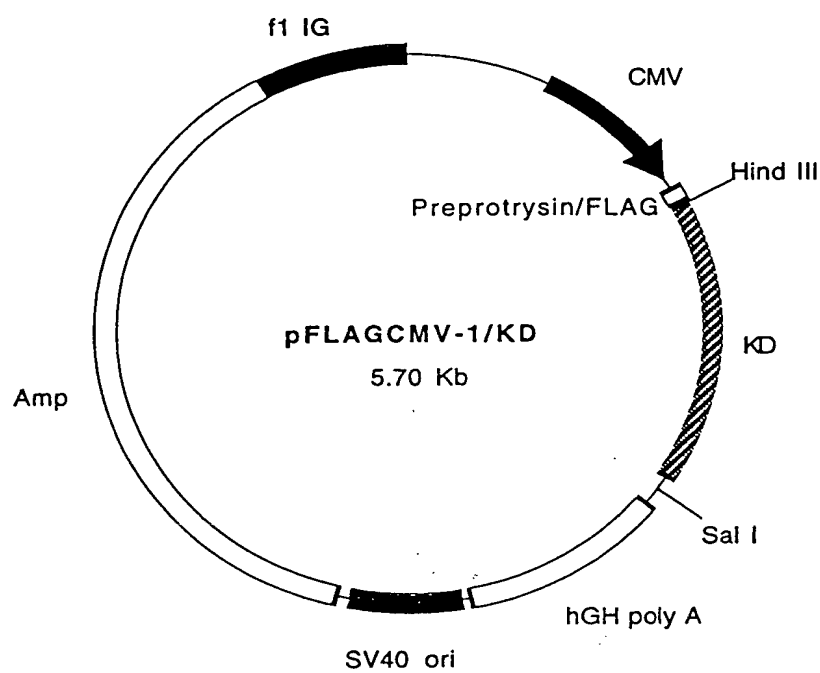


Fig. 3

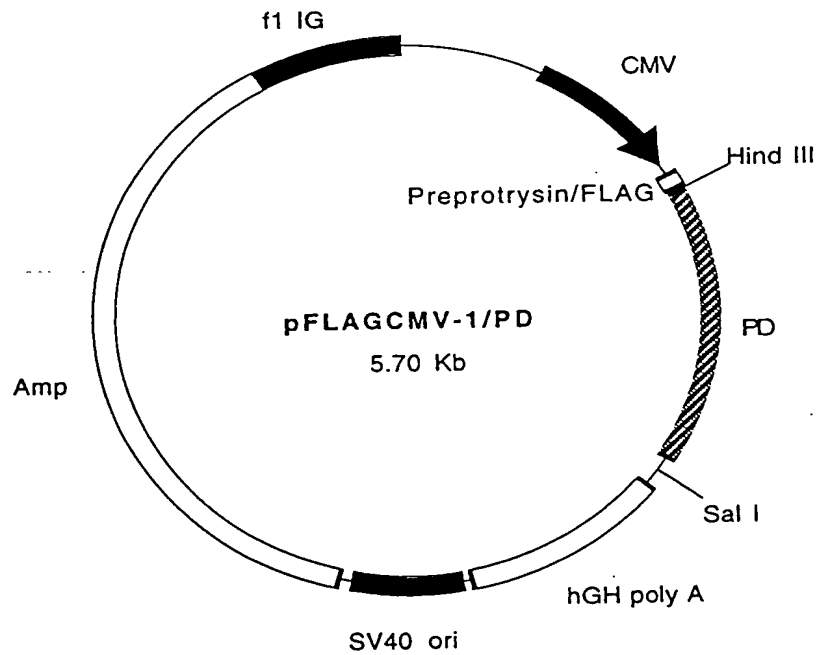
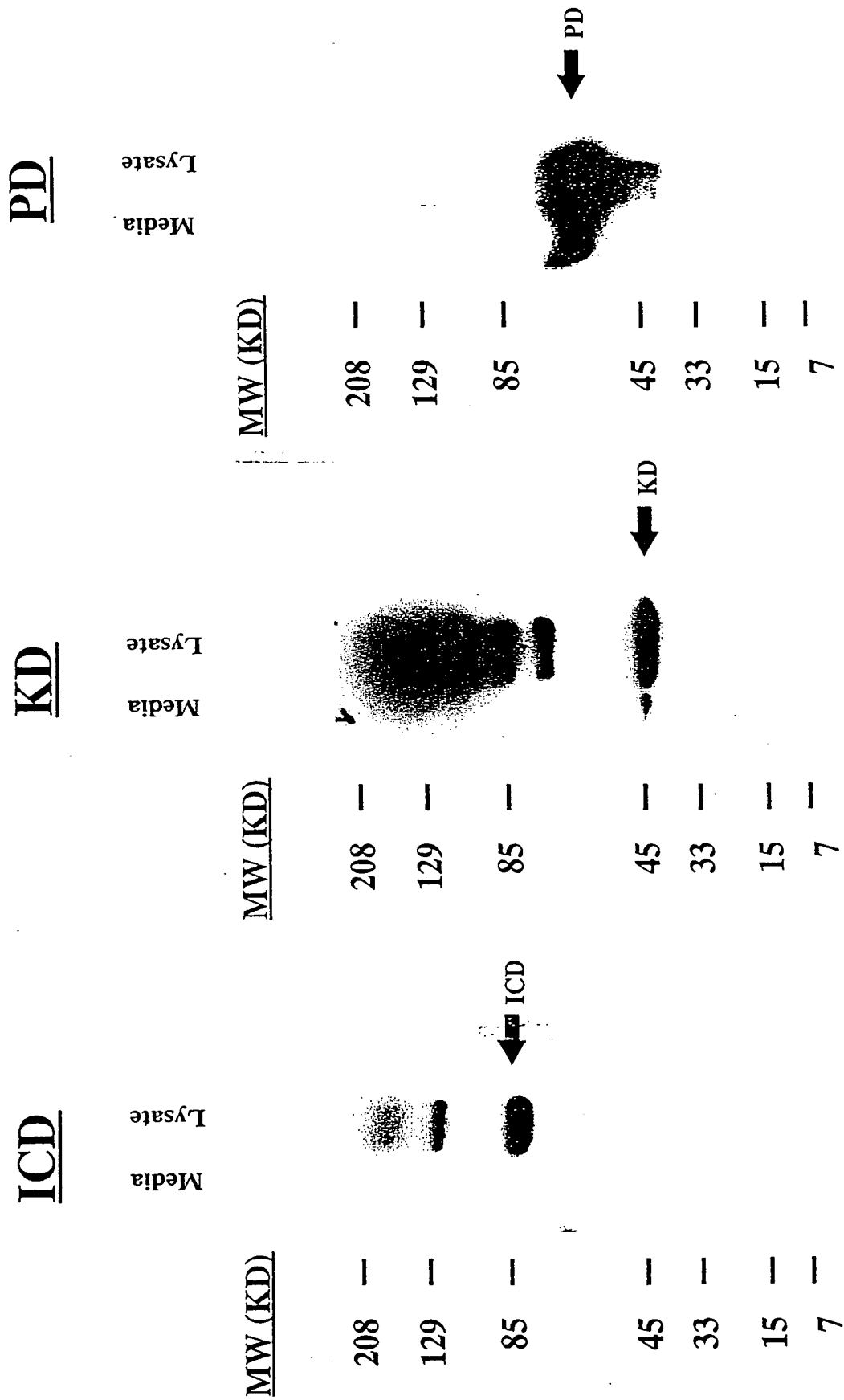


Fig. 4



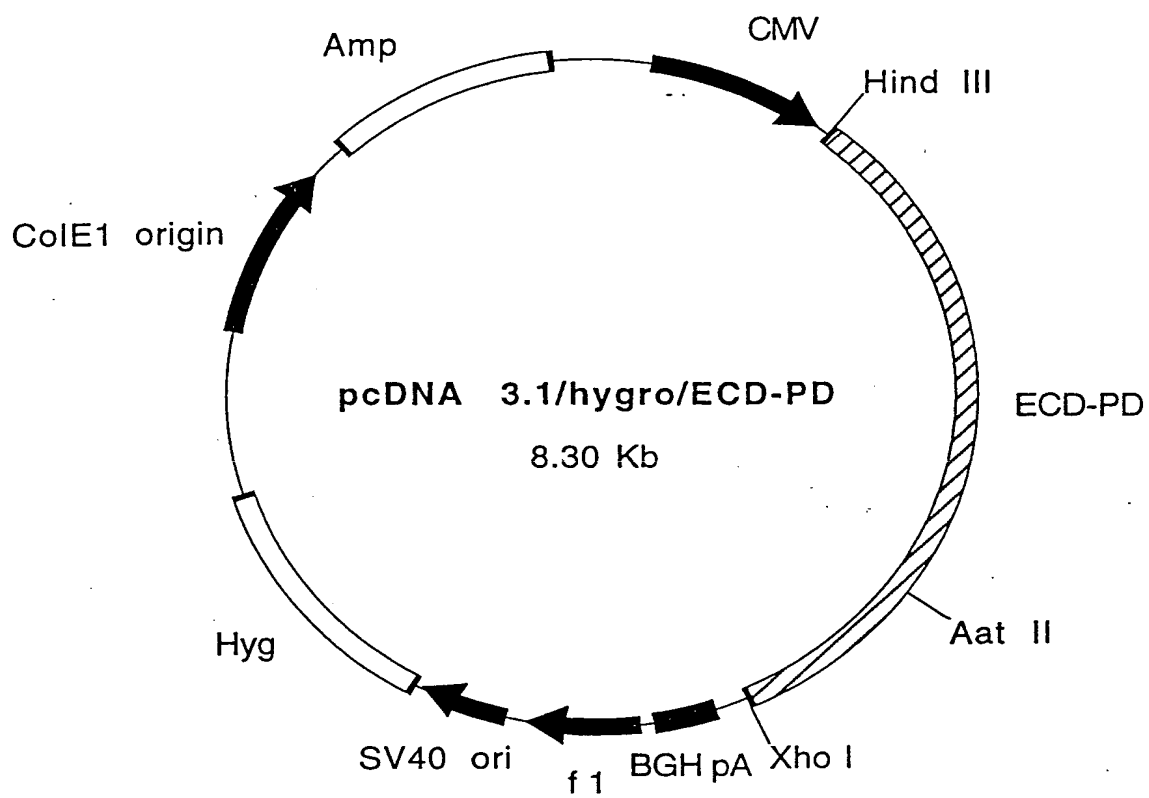
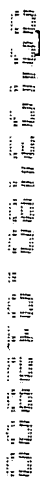


Fig. 5

<u>lysate</u>	<u>Media</u>
pCDNA3.1hyg/ECD-PD	pCDNA3.1hyg/ECD-PD
pFLAGcmv1/PD	pFLAGcmv1/PD
pCDNA3.1hyg	pCDNA3.1hyg
pELAGcmv1/PD	pELAGcmv1/PD
pCDNA3.1hyg	pCDNA3.1hyg
pCDNA3.1hyg/ECD-PD	pCDNA3.1hyg/ECD-PD

[illegible]

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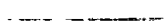


Fig. 7 (SEQ ID NO: 1)

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Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg	Trp	Gly	Leu	Leu	Leu	Ala	Leu	Leu	Pro	Pro	Gly	Ala	20
Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	40
Thr	His	Leu	Asp	Met	Leu	Arg	His	Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	60
Glu	Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val	80
Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu	Gln	Arg	Leu	Arg	100
110										120										
Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	120
Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	140
Gln	Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln	160
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	Asn	Gln	Leu	Ala	180
Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	His	Pro	Cys	Ser	Pro	Met	Cys	Lys	200
210										220										
Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	220
Ala	Gly	Gly	Cys	Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys	240
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	His	Phe	Asn	His	260
Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	280
Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	300
310										320										
Tyr	Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln	320
Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys	Pro	Cys	Ala	Arg	340
Val	Cys	Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu	Val	Arg	Ala	Val	Thr	Ser	Ala	Asn	360
Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys	Lys	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	Ser	380
Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	400
410										420										
Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	Leu	Pro	420
Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	Gly	Arg	Ile	Leu	His	Asn	Gly	Ala	440
Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	Gly	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	460
Leu	Gly	Ser	Gly	Leu	Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val	480
Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr	Ala	Asn	Arg	Pro	500
510										520										
Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His	Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	520
Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	540
Val	Glu	Glu	Cys	Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	Cys	560
Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys	Phe	Gly	Pro	Glu	580
Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp	Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys	600

Fig. 7 (SEQ ID NO: 1)

610										620										
Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	620
Gly	Ala	Cys	Gln	Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys	640
Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser	Ile	Ile	Ser	Ala	Val	Val	Gly	660
Ile	Leu	Leu	Val	Val	Val	Leu	Gly	Val	Val	Phe	Gly	Ile	Leu	Ile	Lys	Arg	Arg	Gln	Gln	680
Lys	Ile	Arg	Lys	Tyr	Thr	Met	Arg	Arg	Leu	Leu	Gln	Glu	Thr	Glu	Leu	Val	Glu	Pro	Leu	700
710										720										
Thr	Pro	Ser	Gly	Ala	Met	Pro	Asn	Gln	Ala	Gln	Met	Arg	Ile	Leu	Lys	Glu	Thr	Glu	Leu	720
Arg	Lys	Val	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys	Gly	Ile	Trp	Ile	740
Pro	Asp	Gly	Glu	Asn	Val	Lys	Ile	Pro	Val	Ala	Ile	Lys	Val	Leu	Arg	Glu	Asn	Thr	Ser	760
Pro	Lys	Ala	Asn	Lys	Glu	Ile	Leu	Asp	Glu	Ala	Tyr	Val	Met	Ala	Gly	Val	Gly	Ser	Pro	780
Tyr	Val	Ser	Arg	Leu	Leu	Gly	Ile	Cys	Leu	Thr	Ser	Thr	Val	Gln	Leu	Val	Thr	Gln	Leu	800
810										820										
Met	Pro	Tyr	Gly	Cys	Leu	Leu	Asp	His	Val	Arg	Glu	Asn	Arg	Gly	Arg	Leu	Gly	Ser	Gln	820
Asp	Leu	Leu	Asn	Trp	Cys	Met	Gln	Ile	Ala	Lys	Gly	Met	Ser	Tyr	Leu	Glu	Asp	Val	Arg	840
Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Lys	Ser	Pro	Asn	His	Val	Lys	860
Ile	Thr	Asp	Phe	Gly	Leu	Ala	Arg	Leu	Leu	Asp	Ile	Asp	Glu	Thr	Glu	Tyr	His	Ala	Asp	880
Gly	Gly	Lys	Val	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Ser	Ile	Leu	Arg	Arg	Arg	Phe	Thr	900
910										920										
His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	Val	Trp	Glu	Leu	Met	Thr	Phe	Gly	Ala	920
Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Ala	Arg	Glu	Ile	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu	Arg	940
Leu	Pro	Gln	Pro	Pro	Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Ile	Met	Val	Lys	Cys	Trp	Met	960
Ile	Asp	Ser	Glu	Cys	Arg	Pro	Arg	Phe	Arg	Glu	Leu	Val	Ser	Glu	Phe	Ser	Arg	Met	Ala	980
Arg	Asp	Pro	Gln	Arg	Phe	Val	Val	Ile	Gln	Asn	Glu	Asp	Leu	Gly	Pro	Ala	Ser	Pro	Leu	1000
1010										1020										
Asp	Ser	Thr	Phe	Tyr	Arg	Ser	Leu	Leu	Glu	Asp	Asp	Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	1020
Glu	Glu	Tyr	Leu	Val	Pro	Gln	Gln	Gly	Phe	Phe	Cys	Pro	Asp	Pro	Ala	Pro	Gly	Ala	Gly	1040
Gly	Met	Val	His	His	Arg	His	Arg	Ser	Ser	Ser	Thr	Arg	Ser	Gly	Gly	Gly	Asp	Leu	Thr	1060
Leu	Gly	Leu	Glu	Pro	Ser	Glu	Glu	Glu	Ala	Pro	Arg	Ser	Pro	Leu	Ala	Pro	Ser	Glu	Gly	1080
Ala	Gly	Ser	Asp	Val	Phe	Asp	Gly	Asp	Leu	Gly	Met	Gly	Ala	Ala	Lys	Gly	Leu	Gln	Ser	1100
1110										1120										
Leu	Pro	Thr	His	Asp	Pro	Ser	Pro	Leu	Gln	Arg	Tyr	Ser	Glu	Asp	Pro	Thr	Val	Pro	Leu	1120
Pro	Ser	Glu	Thr	Asp	Gly	Tyr	Val	Ala	Pro	Leu	Thr	Cys	Ser	Pro	Gln	Pro	Glu	Tyr	Val	1140
Asn	Gln	Pro	Asp	Val	Arg	Pro	Gln	Pro	Pro	Ser	Pro	Arg	Glu	Gly	Pro	Leu	Pro	Ala	Ala	1160
Arg	Pro	Ala	Gly	Ala	Thr	Leu	Glu	Arg	Pro	Lys	Thr	Leu	Ser	Pro	Gly	Lys	Asn	Gly	Val	1180
Val	Lys	Asp	Val	Phe	Ala	Phe	Gly	Gly	Ala	Val	Glu	Asn	Pro	Glu	Tyr	Leu	Thr	Pro	Gln	1200
1210										1220										
Gly	Gly	Ala	Ala	Pro	Gln	Pro	His	Pro	Pro	Pro	Ala	Phe	Ser	Pro	Ala	Phe	Asp	Asn	Leu	1220
Tyr	Tyr	Trp	Asp	Gln	Asp	Pro	Pro	Glu	Arg	Gly	Ala	Pro	Pro	Ser	Thr	Phe	Lys	Gly	Thr	1240
Pro	Thr	Ala	Glu	Asn	Pro	Glu	Tyr	Leu	Gly	Leu	Asp	Val	Pro	Val	1257

Fig. 8 (SEQ ID NO: 2)

										10										20									
Met	Glu	Leu	Ala	Ala	Trp	Cys	Arg	Trp	Gly	Phe	Leu	Leu	Ala	Leu	Leu	Pro	Pro	Gly	Ile	20									
Ala	Gly	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	40									
Thr	His	Leu	Asp	Met	Leu	Arg	His	Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	60									
Glu	Leu	Thr	Tyr	Val	Pro	Ala	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val	80									
Gln	Gly	Tyr	Met	Leu	Ile	Ala	His	Asn	Gln	Val	Lys	Arg	Val	Pro	Leu	Gln	Arg	Leu	Arg	100									
										110										120									
Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Lys	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Arg	120									
Asp	Pro	Gln	Asp	Asn	Val	Ala	Ala	Ser	Thr	Pro	Gly	Arg	Thr	Pro	Glu	Gly	Leu	Arg	Glu	140									
Leu	Gln	Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Arg	Gly	Asn	Pro	160									
Gln	Leu	Cys	Tyr	Gln	Asp	Met	Val	Leu	Trp	Lys	Asp	Val	Phe	Arg	Lys	Asn	Asn	Gln	Leu	180									
Ala	Pro	Val	Asp	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	Pro	Pro	Cys	Ala	Pro	Ala	Cys	200									
										210										220									
Lys	Asp	Asn	His	Cys	Trp	Gly	Glu	Ser	Pro	Glu	Asp	Cys	Gln	Ile	Leu	Thr	Gly	Thr	Ile	220									
Cys	Thr	Ser	Gly	Cys	Ala	Arg	Cys	Lys	Gly	Arg	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	240									
Cys	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	His	Phe	Asn	260									
His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	280									
Glu	Ser	Met	His	Asn	Pro	Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Thr	Cys	300									
										310										320									
Pro	Tyr	Asn	Tyr	Leu	Ser	Thr	Glu	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Pro	Asn	Asn	320									
Gln	Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys	Pro	Cys	Ala	340									
Arg	Val	Cys	Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Gly	Ala	Arg	Ala	Ile	Thr	Ser	Asp	360									
Asn	Val	Gln	Glu	Phe	Asp	Gly	Cys	Lys	Lys	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	380									
Ser	Phe	Asp	Gly	Asp	Pro	Ser	Ser	Gly	Ile	Ala	Pro	Leu	Arg	Pro	Glu	Gln	Leu	Gln	Val	400									
										410										420									
Phe	Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	Leu	420									
Arg	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Arg	Ile	Ile	Arg	Gly	Arg	Ile	Leu	His	Asp	Gly	440									
Ala	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	Gly	Ile	His	Ser	Leu	Gly	Leu	Arg	Ser	Leu	Arg	460									
Glu	Leu	Gly	Ser	Gly	Leu	Ala	Leu	Ile	His	Arg	Asn	Ala	His	Leu	Cys	Phe	Val	His	Thr	480									
Val	Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Ser	Gly	Asn	Arg	500									
										510										520									
Pro	Glu	Glu	Asp	Cys	Gly	Leu	Glu	Gly	Leu	Val	Cys	Asn	Ser	Leu	Cys	Ala	His	Gly	His	520									
Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	Val	Asn	Cys	Ser	His	Phe	Leu	Arg	Gly	Gln	Glu	540									
Cys	Val	Glu	Glu	Cys	Arg	Val	Trp	Lys	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Ser	Asp	Lys	Arg	560									
Cys	Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Ser	Ser	Glu	Thr	Cys	Phe	Gly	Ser	580									
Glu	Ala	Asp	Gln	Cys	Ala	Ala	Cys	Ala	His	Tyr	Lys	Asp	Ser	Ser	Ser	Cys	Val	Ala	Arg	600									

Fig. 8 (SEQ ID NO: 2)

																				610																					620
Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	Tyr	Pro	Asp	Glu	620																					
Glu	Gly	Ile	Cys	Gln	Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Glu	640																					
Arg	Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Val	Thr	Phe	Ile	Ile	Ala	Thr	Val	Val	660																					
Gly	Val	Leu	Leu	Phe	Leu	Ile	Leu	Val	Val	Val	Val	Gly	Ile	Leu	Ile	Lys	Arg	Arg	Arg	680																					
Gln	Lys	Ile	Arg	Lys	Tyr	Thr	Met	Arg	Arg	Leu	Leu	Gln	Glu	Thr	Glu	Leu	Val	Glu	Pro	700																					
																				710																					720
Leu	Thr	Pro	Ser	Gly	Ala	Met	Pro	Asn	Gln	Ala	Gln	Met	Arg	Ile	Leu	Lys	Glu	Thr	Glu	720																					
Leu	Arg	Lys	Val	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys	Gly	Ile	Trp	740																					
Ile	Pro	Asp	Gly	Glu	Asn	Val	Lys	Ile	Pro	Val	Ala	Ile	Lys	Val	Leu	Arg	Glu	Asn	Thr	760																					
Ser	Pro	Lys	Ala	Asn	Lys	Glu	Ile	Leu	Asp	Glu	Ala	Tyr	Val	Met	Ala	Gly	Val	Gly	Ser	780																					
Pro	Tyr	Val	Ser	Arg	Leu	Leu	Gly	Ile	Cys	Leu	Thr	Ser	Thr	Val	Gln	Leu	Val	Thr	Gln	800																					
																				810																					820
Leu	Met	Pro	Tyr	Gly	Cys	Leu	Leu	Asp	His	Val	Arg	Glu	His	Arg	Gly	Arg	Leu	Gly	Ser	820																					
Gln	Asp	Leu	Leu	Asn	Trp	Cys	Val	Gln	Ile	Ala	Lys	Gly	Met	Ser	Tyr	Leu	Glu	Asp	Val	840																					
Arg	Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Lys	Ser	Pro	Asn	His	Val	860																					
Lys	Ile	Thr	Asp	Phe	Gly	Leu	Ala	Arg	Leu	Leu	Asp	Ile	Asp	Glu	Thr	Glu	Tyr	His	Ala	880																					
Asp	Gly	Gly	Lys	Val	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Ser	Ile	Leu	Arg	Arg	Arg	Phe	900																					
																				910																					920
Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	Val	Trp	Glu	Leu	Met	Thr	Phe	Gly	920																					
Ala	Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Ala	Arg	Glu	Ile	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu	940																					
Arg	Leu	Pro	Gln	Pro	Pro	Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Ile	Met	Val	Lys	Cys	Trp	960																					
Met	Ile	Asp	Ser	Glu	Cys	Arg	Pro	Arg	Phe	Arg	Glu	Leu	Val	Ser	Glu	Phe	Ser	Arg	Met	980																					
Ala	Arg	Asp	Pro	Gln	Arg	Phe	Val	Val	Ile	Gln	Asn	Glu	Asp	Leu	Gly	Pro	Ser	Ser	Pro	1000																					
																				1010																					1020
Met	Asp	Ser	Thr	Phe	Tyr	Arg	Ser	Leu	Leu	Glu	Asp	Asp	Asp	Met	Gly	Asp	Leu	Val	Asp	1020																					
Ala	Glu	Glu	Tyr	Leu	Val	Pro	Gln	Gln	Gly	Phe	Phe	Ser	Pro	Asp	Pro	Thr	Pro	Gly	Thr	1040																					
Gly	Ser	Thr	Ala	His	Arg	Arg	His	Arg	Ser	Ser	Ser	Thr	Arg	Ser	Gly	Gly	Gly	Glu	Leu	1060																					
Thr	Leu	Gly	Leu	Glu	Pro	Ser	Glu	Glu	Gly	Pro	Pro	Arg	Ser	Pro	Leu	Ala	Pro	Ser	Glu	1080																					
Gly	Ala	Gly	Ser	Asp	Val	Phe	Asp	Gly	Asp	Leu	Ala	Met	Gly	Val	Thr	Lys	Gly	Leu	Gln	1100																					
																				1110																					1120
Ser	Leu	Ser	Pro	His	Asp	Leu	Ser	Pro	Leu	Gln	Arg	Tyr	Ser	Glu	Asp	Pro	Thr	Leu	Pro	1120																					
Leu	Pro	Pro	Glu	Thr	Asp	Gly	Tyr	Val	Ala	Pro	Leu	Ala	Cys	Ser	Pro	Gln	Pro	Glu	Tyr	1140																					
Val	Asn	Gln	Ser	Glu	Val	Gln	Pro	Gln	Pro	Pro	Leu	Thr	Pro	Glu	Gly	Pro	Leu	Pro	Pro	1160																					
Val	Arg	Pro	Ala	Gly	Ala	Thr	Leu	Glu	Arg	Pro	Lys	Thr	Leu	Ser	Pro	Gly	Lys	Asn	Gly	1180																					
Val	Val	Lys	Asp	Val	Phe	Ala	Phe	Gly	Gly	Ala	Val	Glu	Asn	Pro	Glu	Tyr	Leu	Val	Pro	1200																					
																				1210																					1220
Arg	Glu	Gly	Thr	Ala	Ser	Pro	Pro	His	Pro	Ser	Pro	Ala	Phe	Ser	Pro	Ala	Phe	Asp	Asn	1220																					
Leu	Tyr	Tyr	Trp	Asp	Gln	Asn	Ser	Ser	Glu	Gln	Gly	Pro	Pro	Pro	Ser	Asn	Phe	Glu	Gly	1240																					
Thr	Pro	Thr	Ala	Glu	Asn	Pro	Glu	Tyr	Leu	Gly	Leu	Asp	Val	Pro	Val	1258																					

Fig. 9 (SEQ ID NO: 3)

																			10																				20
Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg	Trp	Gly	Leu	Leu	Leu	Ala	Leu	Leu	Pro	Pro	Gly	Ala	20																			
Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	40																			
Thr	His	Leu	Asp	Met	Leu	Arg	His	Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	60																			
Glu	Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val	80																			
Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu	Gln	Arg	Leu	Arg	100																			
																			110																				120
Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	120																			
Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	140																			
Gln	Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln	160																			
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	Asn	Gln	Leu	Ala	180																			
Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	His	Pro	Cys	Ser	Pro	Met	Cys	Lys	200																			
																			210																				220
Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	220																			
Ala	Gly	Gly	Cys	Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys	240																			
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	His	Phe	Asn	His	260																			
Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	280																			
Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	300																			
																			310																				320
Tyr	Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln	320																			
Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys	Pro	Cys	Ala	Arg	340																			
Val	Cys	Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu	Val	Arg	Ala	Val	Thr	Ser	Ala	Asn	360																			
Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys	Lys	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	Ser	380																			
Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	400																			
																			410																				420
Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	Leu	Pro	420																			
Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	Gly	Arg	Ile	Leu	His	Asn	Gly	Ala	440																			
Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	Gly	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	460																			
Leu	Gly	Ser	Gly	Leu	Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val	480																			
Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr	Ala	Asn	Arg	Pro	500																			
																			510																				520
Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His	Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	520																			
Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	540																			
Val	Glu	Glu	Cys	Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	Cys	560																			
Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys	Phe	Gly	Pro	Glu	580																			
Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp	Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys	600																			
																			610																				620
Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	620																			
Gly	Ala	Cys	Gln	Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys	640																			
Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser	653																										

Fig. 10 (SEQ ID NO: 4)

[illegible]

Fig. 11 (SEQ ID NO: 5)

																			10																				20
Gln	Asn	Glu	Asp	Leu	Gly	Pro	Ala	Ser	Pro	Leu	Asp	Ser	Thr	Phe	Tyr	Arg	Ser	Leu	Leu	20																			
Glu	Asp	Asp	Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	Glu	Glu	Tyr	Leu	Val	Pro	Gln	Gln	Gly	40																			
Phe	Phe	Cys	Pro	Asp	Pro	Ala	Pro	Gly	Ala	Gly	Gly	Met	Val	His	His	Arg	His	Arg	.	60																			

Fig. 12 (SEQ ID NO: 6)

										10											20
Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg	Trp	Gly	Leu	Leu	Leu	Ala	Leu	Leu	Pro	Pro	Gly	Ala		20
Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu		40
Thr	His	Leu	Asp	Met	Leu	Arg	His	Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu		60
Glu	Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val		80
Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu	Gln	Arg	Leu	Arg		100
										110											120
Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly		120
Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu		140
Gln	Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln		160
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	Asn	Gln	Leu	Ala		180
Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	His	Pro	Cys	Ser	Pro	Met	Cys	Lys		200
										210											220
Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys		220
Ala	Gly	Gly	Cys	Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys		240
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	His	Phe	Asn	His		260
Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu		280
Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro		300
										310											320
Tyr	Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln		320
Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys	Pro	Cys	Ala	Arg		340
Val	Cys	Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu	Val	Arg	Ala	Val	Thr	Ser	Ala	Asn		360
Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys	Lys	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	Ser		380
Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe		400
										410											420
Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	Leu	Pro		420
Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	Gly	Arg	Ile	Leu	His	Asn	Gly	Ala		440
Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	Gly	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu		460
Leu	Gly	Ser	Gly	Leu	Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val		480
Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr	Ala	Asn	Arg	Pro		500
										510											520
Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His	Gln	Leu	Cys	Ala	Arg	Gly	His	Cys		520
Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys		540
Val	Glu	Glu	Cys	Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	Cys		560
Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys	Phe	Gly	Pro	Glu		580
Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp	Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys		600

Fig. 12 (SEQ ID NO: 6)

610															620					
Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	620
Gly	Ala	Cys	Gln	Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys	640
Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser	Gln	Asn	Glu	Asp	Leu	Gly	Pro	660
Ala	Ser	Pro	Leu	Asp	Ser	Thr	Phe	Tyr	Arg	Ser	Leu	Leu	Glu	Asp	Asp	Asp	Met	Gly	Asp	680
Leu	Val	Asp	Ala	Glu	Glu	Tyr	Leu	Val	Pro	Gln	Gln	Gly	Phe	Phe	Cys	Pro	Asp	Pro	Ala	700
710															720					
Pro	Gly	Ala	Gly	Gly	Met	Val	His	His	Arg	His	Arg	Ser	Ser	Ser	Thr	Arg	Ser	Gly	Gly	720
Gly	Asp	Leu	Thr	Leu	Gly	Leu	Glu	Pro	Ser	Glu	Glu	Glu	Ala	Pro	Arg	Ser	Pro	Leu	Ala	740
Pro	Ser	Glu	Gly	Ala	Gly	Ser	Asp	Val	Phe	Asp	Gly	Asp	Leu	Gly	Met	Gly	Ala	Ala	Lys	760
Gly	Leu	Gln	Ser	Leu	Pro	Thr	His	Asp	Pro	Ser	Pro	Leu	Gln	Arg	Tyr	Ser	Glu	Asp	Pro	780
Thr	Val	Pro	Leu	Pro	Ser	Glu	Thr	Asp	Gly	Tyr	Val	Ala	Pro	Leu	Thr	Cys	Ser	Pro	Gln	800
810															820					
Pro	Glu	Tyr	Val	Asn	Gln	Pro	Asp	Val	Arg	Pro	Gln	Pro	Pro	Ser	Pro	Arg	Glu	Gly	Pro	820
Leu	Pro	Ala	Ala	Arg	Pro	Ala	Gly	Ala	Thr	Leu	Glu	Arg	Pro	Lys	Thr	Leu	Ser	Pro	Gly	840
Lys	Asn	Gly	Val	Val	Lys	Asp	Val	Phe	Ala	Phe	Gly	Gly	Ala	Val	Glu	Asn	Pro	Glu	Tyr	860
Leu	Thr	Pro	Gln	Gly	Gly	Ala	Ala	Pro	Gln	Pro	His	Pro	Pro	Pro	Ala	Phe	Ser	Pro	Ala	880
Phe	Asp	Asn	Leu	Tyr	Tyr	Trp	Asp	Gln	Asp	Pro	Pro	Glu	Arg	Gly	Ala	Pro	Pro	Ser	Thr	900
910															920					
Phe	Lys	Gly	Thr	Pro	Thr	Ala	Glu	Asn	Pro	Glu	Tyr	Leu	Gly	Leu	Asp	Val	Pro	Val	.	920

Fig. 14 (SEQ ID NO: 8)

10										20										
Met	Glu	Leu	Ala	Ala	Trp	Cys	Arg	Trp	Gly	Phe	Leu	Leu	Ala	Leu	Leu	Pro	Pro	Gly	Ile	20
Ala	Gly	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	40
Thr	His	Leu	Asp	Met	Leu	Arg	His	Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	60
Glu	Leu	Thr	Tyr	Val	Pro	Ala	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val	80
Gln	Gly	Tyr	Met	Leu	Ile	Ala	His	Asn	Gln	Val	Lys	Arg	Val	Pro	Leu	Gln	Arg	Leu	Arg	100
110										120										
Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Lys	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Arg	120
Asp	Pro	Gln	Asp	Asn	Val	Ala	Ala	Ser	Thr	Pro	Gly	Arg	Thr	Pro	Glu	Gly	Leu	Arg	Glu	140
Leu	Gln	Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Arg	Gly	Asn	Pro	160
Gln	Leu	Cys	Tyr	Gln	Asp	Met	Val	Leu	Trp	Lys	Asp	Val	Phe	Arg	Lys	Asn	Asn	Gln	Leu	180
Ala	Pro	Val	Asp	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	Pro	Pro	Cys	Ala	Pro	Ala	Cys	200
210										220										
Lys	Asp	Asn	His	Cys	Trp	Gly	Glu	Ser	Pro	Glu	Asp	Cys	Gln	Ile	Leu	Thr	Gly	Thr	Ile	220
Cys	Thr	Ser	Gly	Cys	Ala	Arg	Cys	Lys	Gly	Arg	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	240
Cys	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	His	Phe	Asn	260
His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	280
Glu	Ser	Met	His	Asn	Pro	Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Thr	Cys	300
310										320										
Pro	Tyr	Asn	Tyr	Leu	Ser	Thr	Glu	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Pro	Asn	Asn	320
Gln	Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys	Pro	Cys	Ala	340
Arg	Val	Cys	Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Gly	Ala	Arg	Ala	Ile	Thr	Ser	Asp	360
Asp	Val	Gln	Glu	Phe	Asp	Gly	Cys	Lys	Lys	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	380
Ser	Phe	Asp	Gly	Asp	Pro	Ser	Ser	Gly	Ile	Ala	Pro	Leu	Arg	Pro	Glu	Gln	Leu	Gln	Val	400
410										420										
Phe	Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	Leu	420
Arg	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Arg	Ile	Ile	Arg	Gly	Arg	Ile	Leu	His	Asp	Gly	440
Ala	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	Gly	Ile	His	Ser	Leu	Gly	Leu	Arg	Ser	Leu	Arg	460
Glu	Leu	Gly	Ser	Gly	Leu	Ala	Leu	Ile	His	Arg	Asn	Ala	His	Leu	Cys	Phe	Val	His	Thr	480
Val	Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Ser	Gly	Asn	Arg	500
510										520										
Pro	Glu	Glu	Asp	Cys	Gly	Leu	Glu	Gly	Leu	Val	Cys	Asn	Ser	Leu	Cys	Ala	His	Gly	His	520
Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	Val	Asn	Cys	Ser	His	Phe	Leu	Arg	Gly	Gln	Glu	540
Cys	Val	Glu	Glu	Cys	Arg	Val	Trp	Lys	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Ser	Asp	Lys	Arg	560
Cys	Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Ser	Ser	Glu	Thr	Cys	Phe	Gly	Ser	580
Glu	Ala	Asp	Gln	Cys	Ala	Ala	Cys	Ala	His	Tyr	Lys	Asp	Ser	Ser	Ser	Cys	Val	Ala	Arg	600
610										620										
Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	Tyr	Pro	Asp	Glu	620
Glu	Gly	Ile	Cys	Gln	Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Glu	640
Arg	Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Val	Thr	Phe							654

Fig. 15 (SEQ ID NO: 9)

ATG GAG CTG GCG GCC TTG TGC CGC TGG GGG CTC CTC CTC GCC CTC TTG	48
Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu	
1 5 10 15	
CCC CCC GGA GCC GCG AGC ACC CAA GTG TGC ACC GGC ACA GAC ATG AAG	96
Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys	
20 25 30	
CTG CGG CTC CCT GCC AGT CCC GAG ACC CAC CTG GAC ATG CTC CGC CAC	144
Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His	
35 40 45	
CTC TAC CAG GGC TGC CAG GTG GTG CAG GGA AAC CTG GAA CTC ACC TAC	192
Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr	
50 55 60	
CTG CCC ACC AAT GCC AGC CTG TCC TTC CTG CAG GAT ATC CAG GAG GTG	240
Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val	
65 70 75 80	
CAG GGC TAC GTG CTC ATC GCT CAC AAC CAA GTG AGG CAG GTC CCA CTG	288
Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu	
85 90 95	
CAG AGG CTG CGG ATT GTG CGA GGC ACC CAG CTC TTT GAG GAC AAC TAT	336
Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr	
100 105 110	
GCC CTG GCC GTG CTA GAC AAT GGA GAC CCG CTG AAC AAT ACC ACC CCT	384
Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro	
115 120 125	

Fig. 15 (SEQ ID NO: 9)

GTC	ACA	GGG	GCC	TCC	CCA	GGA	GGC	CTG	CGG	GAG	CTG	CAG	CTT	CGA	AGC	432
Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser	
130						135					140					
CTC	ACA	GAG	ATC	TTG	AAA	GGA	GGG	GTC	TTG	ATC	CAG	CGG	AAC	CCC	CAG	480
Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln	
145					150					155					160	
CTC	TGC	TAC	CAG	GAC	ACG	ATT	TTG	TGG	AAG	GAC	ATC	TTC	CAC	AAG	AAC	528
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	
				165					170					175		
AAC	CAG	CTG	GCT	CTC	ACA	CTG	ATA	GAC	ACC	AAC	CGC	TCT	CGG	GCC	TGC	576
Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	
			180					185					190			
CAC	CCC	TGT	TCT	CCG	ATG	TGT	AAG	GGC	TCC	CGC	TGC	TGG	GGA	GAG	AGT	624
His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	
		195					200					205				
TCT	GAG	GAT	TGT	CAG	AGC	CTG	ACG	CGC	ACT	GTC	TGT	GCC	GGT	GGC	TGT	672
Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys	
	210					215					220					
GCC	CGC	TGC	AAG	GGG	CCA	CTG	CCC	ACT	GAC	TGC	TGC	CAT	GAG	CAG	TGT	720
Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys	
225					230					235					240	
GCT	GCC	GGC	TGC	ACG	GGC	CCC	AAG	CAC	TCT	GAC	TGC	CTG	GCC	TGC	CTC	768
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	
				245					250					255		
CAC	TTC	AAC	CAC	AGT	GGC	ATC	TGT	GAG	CTG	CAC	TGC	CCA	GCC	CTG	GTC	816
His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	
			260					265					270			
ACC	TAC	AAC	ACA	GAC	ACG	TTT	GAG	TCC	ATG	CCC	AAT	CCC	GAG	GGC	CGG	864
Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg	
		275					280					285				
TAT	ACA	TTC	GGC	GCC	AGC	TGT	GTG	ACT	GCC	TGT	CCC	TAC	AAC	TAC	CTT	912
Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu	
	290					295					300					

Fig. 15 (SEQ ID NO: 9)

TCT ACG GAC GTG GGA TCC TGC ACC CTC GTC TGC CCC CTG CAC AAC CAA	960
Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln	
305 310 315 320	
GAG GTG ACA GCA GAG GAT GGA ACA CAG CGG TGT GAG AAG TGC AGC AAG	1008
Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys	
325 330 335	
CCC TGT GCC CGA GTG TGC TAT GGT CTG GGC ATG GAG CAC TTG CGA GAG	1056
Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu	
340 345 350	
GTG AGG GCA GTT ACC AGT GCC AAT ATC CAG GAG TTT GCT GGC TGC AAG	1104
Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys	
355 360 365	
AAG ATC TTT GGG AGC CTG GCA TTT CTG CCG GAG AGC TTT GAT GGG GAC	1152
Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp	
370 375 380	
CCA GCC TCC AAC ACT GCC CCG CTC CAG CCA GAG CAG CTC CAA GTG TTT	1200
Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe	
385 390 395 400	
GAG ACT CTG GAA GAG ATC ACA GGT TAC CTA TAC ATC TCA GCA TGG CCG	1248
Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro	
405 410 415	
GAC AGC CTG CCT GAC CTC AGC GTC TTC CAG AAC CTG CAA GTA ATC CGG	1296
Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg	
420 425 430	
GGA CGA ATT CTG CAC AAT GGC GCC TAC TCG CTG ACC CTG CAA GGG CTG	1344
Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu	
435 440 445	
GGC ATC AGC TGG CTG GGG CTG CGC TCA CTG AGG GAA CTG GGC AGT GGA	1392
Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly	
450 455 460	
CTG GCC CTC ATC CAC CAT AAC ACC CAC CTC TGC TTC GTG CAC ACG GTG	1440
Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val	
465 470 475 480	

[illegible]

CCC Pro	TGG Trp	GAC Asp	CAG Gln	CTC Leu 485	TTT Phe	CGG Arg	AAC Asn	CCG Pro	CAC His 490	CAA Gln	GCT Ala	CTG Leu	CTC Leu	CAC His 495	ACT Thr	1488
GCC Ala	AAC Asn	CGG Arg	CCA Pro 500	GAG Glu	GAC Asp	GAG Glu	TGT Cys	GTG Val 505	GGC Gly	GAG Glu	GGC Gly	CTG Leu	GCC Ala 510	TGC Cys	CAC His	1536
CAG Gln	CTG Leu	TGC Cys 515	GCC Ala	CGA Arg	GGG Gly	CAC His	TGC Cys 520	TGG Trp	GGT Gly	CCA Pro	GGG Gly	CCC Pro 525	ACC Thr	CAG Gln	TGT Cys	1584
GTC Val 530	AAC Asn	TGC Cys	AGC Ser	CAG Gln	TTC Phe	CTT Leu 535	CGG Arg	GGC Gly	CAG Gln	GAG Glu	TGC Cys 540	GTG Val	GAG Glu	GAA Glu	TGC Cys	1632
CGA Arg 545	GTA Val	CTG Leu	CAG Gln	GGG Gly	CTC Leu 550	CCC Pro	AGG Arg	GAG Glu	TAT Tyr	GTG Val 555	AAT Asn	GCC Ala	AGG Arg	CAC His	TGT Cys 560	1680
TTG Leu	CCG Pro	TGC Cys	CAC His	CCT Pro 565	GAG Glu	TGT Cys	CAG Gln	CCC Pro 570	CAG Gln	AAT Asn	GGC Gly	TCA Ser	GTG Val	ACC Thr 575	TGT Cys	1728
TTT Phe	GGA Gly	CCG Pro	GAG Glu 580	GCT Ala	GAC Asp	CAG Gln	TGT Cys	GTG Val 585	GCC Ala	TGT Cys	GCC Ala	CAC His	TAT Tyr 590	AAG Lys	GAC Asp	1776
CCT Pro	CCC Pro	TTC Phe 595	TGC Cys	GTG Val	GCC Ala	CGC Arg	TGC Cys 600	CCC Pro	AGC Ser	GGT Gly	GTG Val	AAA Lys 605	CCT Pro	GAC Asp	CTC Leu	1824
TCC Ser	TAC Tyr 610	ATG Met	CCC Pro	ATC Ile	TGG Trp	AAG Lys 615	TTT Phe	CCA Pro	GAT Asp	GAG Glu	GAG Glu 620	GGC Gly	GCA Ala	TGC Cys	CAG Gln	1872
CCT Pro 625	TGC Cys	CCC Pro	ATC Ile	AAC Asn	TGC Cys 630	ACC Thr	CAC His	TCC Ser	TGT Cys	GTG Val 635	GAC Asp	CTG Leu	GAT Asp	GAC Asp	AAG Lys 640	1920
GGC Gly	TGC Cys	CCC Pro	GCC Ala	GAG Glu 645	CAG Gln	AGA Arg	GCC Ala	AGC Ser	CCT Pro 650	CTG Leu	ACG Thr	TCC Ser	ATC Ile	ATC Ile 655	TCT Ser	1968
GCG Ala	GTG Val	GTT Val	GGC Gly 660	ATT Ile	CTG Leu	CTG Leu	GTC Val	GTG Val 665	GTC Val	TTG Leu	GGG Gly	GTG Val 670	GTC Val	TTT Phe	GGG Gly	2016

Fig. 15 (SEQ ID NO: 9)

ATC CTC ATC AAG CGA CGG CAG CAG AAG ATC CGG AAG TAC ACG ATG CGG	2064
Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg	
675 680 685	
AGA CTG CTG CAG GAA ACG GAG CTG GTG GAG CCG CTG ACA CCT AGC GGA	2112
Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly	
690 695 700	
GCG ATG CCC AAC CAG GCG CAG ATG CGG ATC CTG AAA GAG ACG GAG CTG	2160
Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu	
705 710 715 720	
AGG AAG GTG AAG GTG CTT GGA TCT GGC GCT TTT GGC ACA GTC TAC AAG	2208
Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys	
725 730 735	
GGC ATC TGG ATC CCT GAT GGG GAG AAT GTG AAA ATT CCA GTG GCC ATC	2256
Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile	
740 745 750	
AAA GTG TTG AGG GAA AAC ACA TCC CCC AAA GCC AAC AAA GAA ATC TTA	2304
Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu	
755 760 765	
GAC GAA GCA TAC GTG ATG GCT GGT GTG GGC TCC CCA TAT GTC TCC CGC	2352
Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg	
770 775 780	
CTT CTG GGC ATC TGC CTG ACA TCC ACG GTG CAG CTG GTG ACA CAG CTT	2400
Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu	
785 790 795 800	
ATG CCC TAT GGC TGC CTC TTA GAC CAT GTC CGG GAA AAC CGC GGA CGC	2448
Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg	
805 810 815	
CTG GGC TCC CAG GAC CTG CTG AAC TGG TGT ATG CAG ATT GCC AAG GGG	2496
Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly	
820 825 830	
ATG AGC TAC CTG GAG GAT GTG CGG CTC GTA CAC AGG GAC TTG GCC GCT	2544
Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala	
835 840 845	

Fig. 15 (SEQ ID NO: 9)

CGG AAC GTG CTG GTC AAG AGT CCC AAC CAT GTC AAA ATT ACA GAC TTC	2592
Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe	
850 855 860	
GGG CTG GCT CGG CTG CTG GAC ATT GAC GAG ACA GAG TAC CAT GCA GAT	2640
Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp	
865 870 875 880	
GGG GGC AAG GTG CCC ATC AAG TGG ATG GCG CTG GAG TCC ATT CTC CGC	2688
Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg	
885 890 895	
CGG CGG TTC ACC CAC CAG AGT GAT GTG TGG AGT TAT GGT GTG ACT GTG	2736
Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val	
900 905 910	
TGG GAG CTG ATG ACT TTT GGG GCC AAA CCT TAC GAT GGG ATC CCA GCC	2784
Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala	
915 920 925	
CGG GAG ATC CCT GAC CTG CTG GAA AAG GGG GAG CGG CTG CCC CAG CCC	2832
Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro	
930 935 940	
CCC ATC TGC ACC ATT GAT GTC TAC ATG ATC ATG GTC AAA TGT TGG ATG	2880
Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met	
945 950 955 960	
ATT GAC TCT GAA TGT CGG CCA AGA TTC CGG GAG TTG GTG TCT GAA TTC	2928
Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe	
965 970 975	
TCC CGC ATG GCC AGG GAC CCC CAG CGC TTT GTG GTC ATC CAG AAT GAG	2976
Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu	
980 985 990	
GAC TTG GGC CCA GCC AGT CCC TTG GAC AGC ACC TTC TAC CGC TCA CTG	3024
Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu	
995 1000 1005	
CTG GAG GAC GAT GAC ATG GGG GAC CTG GTG GAT GCT GAG GAG TAT CTG	3072
Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu	
1010 1015 1020	

Fig. 15 (SEQ ID NO: 9)

GTA CCC CAG CAG GGC TTC TTC TGT CCA GAC CCT GCC CCG GGC GCT GGG	3120
Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly	
1025 1030 1035 1040	
GGC ATG GTC CAC CAC AGG CAC CGC AGC TCA TCT ACC AGG AGT GGC GGT	3168
Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly	
1045 1050 1055	
GGG GAC CTG ACA CTA GGG CTG GAG CCC TCT GAA GAG GAG GCC CCC AGG	3216
Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro Arg	
1060 1065 1070	
TCT CCA CTG GCA CCC TCC GAA GGG GCT GGC TCC GAT GTA TTT GAT GGT	3264
Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly	
1075 1080 1085	
GAC CTG GGA ATG GGG GCA GCC AAG GGG CTG CAA AGC CTC CCC ACA CAT	3312
Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His	
1090 1095 1100	
GAC CCC AGC CCT CTA CAG CGG TAC AGT GAG GAC CCC ACA GTA CCC CTG	3360
Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu	
1105 1110 1115 1120	
CCC TCT GAG ACT GAT GGC TAC GTT GCC CCC CTG ACC TGC AGC CCC CAG	3408
Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln	
1125 1130 1135	
CCT GAA TAT GTG AAC CAG CCA GAT GTT CGG CCC CAG CCC CCT TCG CCC	3456
Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro	
1140 1145 1150	
CGA GAG GGC CCT CTG CCT GCT GCC CGA CCT GCT GGT GCC ACT CTG GAA	3504
Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu	
1155 1160 1165	
AGG CCC AAG ACT CTC TCC CCA GGG AAG AAT GGG GTC GTC AAA GAC GTT	3552
Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val	
1170 1175 1180	
TTT GCC TTT GGG GGT GCC GTG GAG AAC CCC GAG TAC TTG ACA CCC CAG	3600
Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln	
1185 1190 1195 1200	

Herceptin Binding by Direct Elisa 10/5/99

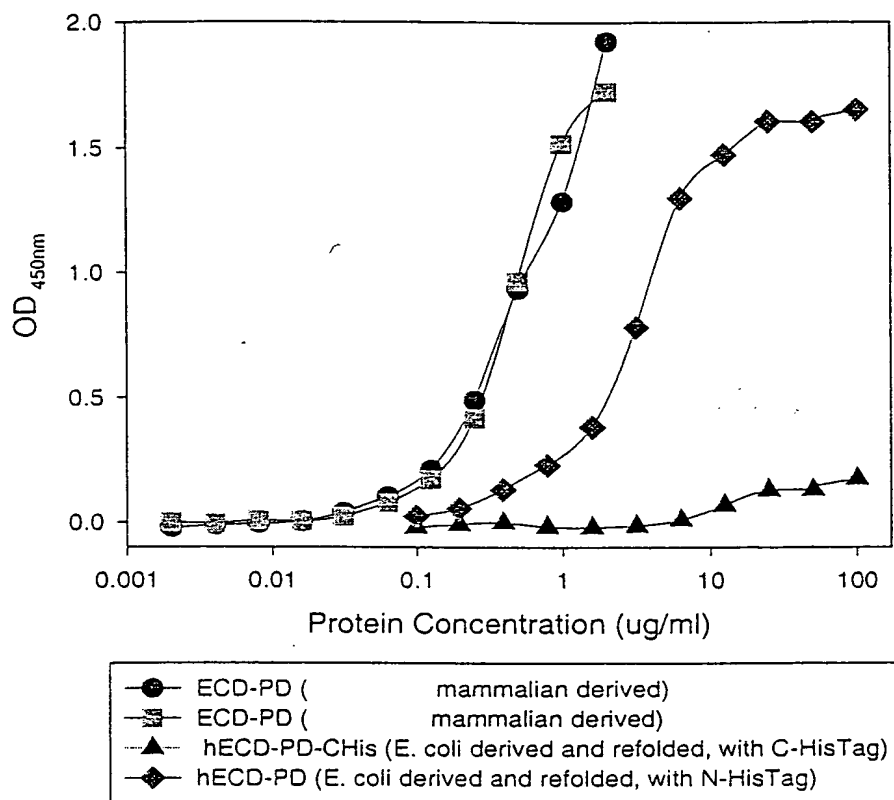
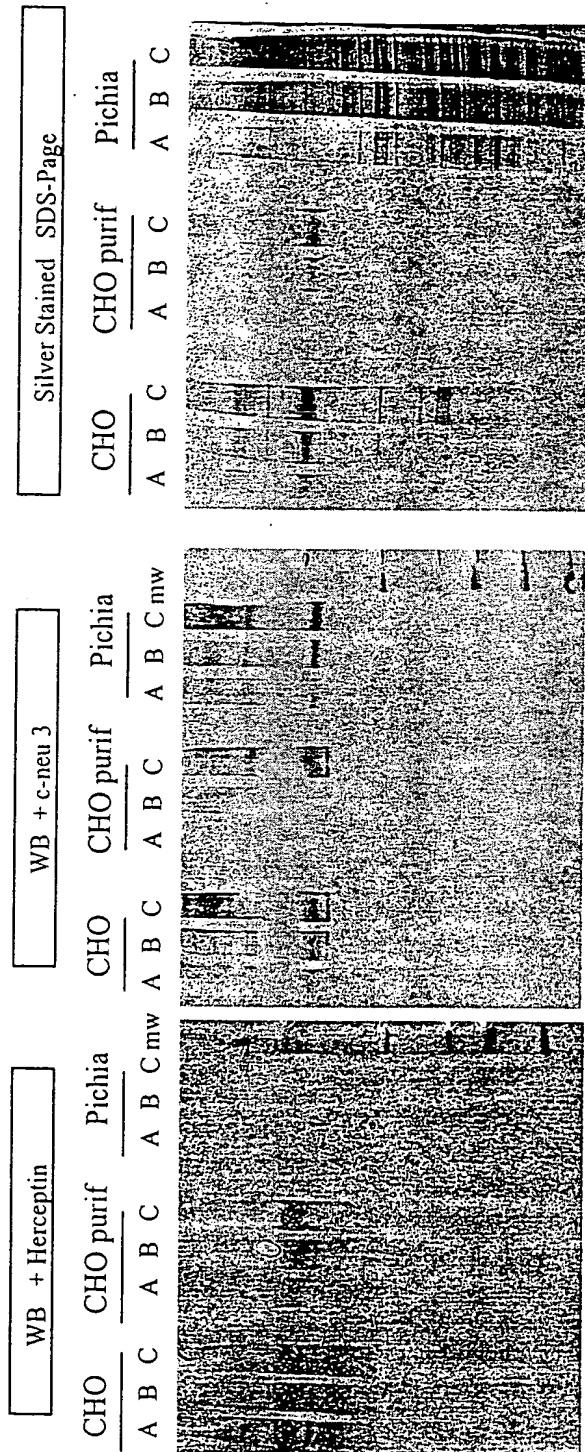


Fig. 17

Comparison of Her2neu ECD-PD Expression in CHO-K1 (S/SF) and Pichia (Non reducing conditions)



Legend : CHO; A, B , C = 2,5µl / 5µl / 10µl

CHO purif; A , B , C = 125ng / 250ng / 500ng

Pichia ; A, B, C = 2,5µl / 5µl / 10µl from a 1/30 dilution of OD 120

Fig. 19 (SEQ ID NO:11)

atggagctgg	cggcctggtg	ccgttggggg	ttcctcctcg	ccctcctgtc	ccccggagcc	60
gcgggtaccc	aagtgtgtac	cggtaccgac	atgaagtgtc	gactccctgc	cagtcctgag	120
accacacctg	acatgcttcg	ccacctctac	cagggctgtc	aggtggtgca	gggcaatttg	180
gagcttacct	acctgcccgc	caatgccagc	ctctcattcc	tgcaggacat	ccaggaagtc	240
cagggataca	tgctcatcgc	tcacaaccga	gtgaaacacg	tcccactgca	gaggttgctc	300
atcgtgagag	ggactcagct	ctttgaggac	aagtatgccc	tggctgtgct	agacaaccga	360
gaccttttgg	acaacgtcac	caccgcccgc	ccaggcagaa	ccccagaagg	gctgcgggag	420
ctgcagcttc	gaagtctcac	agagatcttg	aagggaggag	ttttgatccg	tgggaaccct	480
cagctctgct	accaggacat	ggttttgtgg	aaggatgtcc	tccgtaagaa	taaccagctg	540
gctcctgtcg	acatggacac	caatcgttcc	cgggcctgtc	caccttgtgc	cccaacctgc	600
aaagacaatc	actgttgggg	tgagagtctc	gaagactgtc	agatcttgac	tggcaccatc	660
tgtactagt	gctgtgcccg	gtgcaagggc	cggctgccc	ctgactgttg	ccatgagcag	720
tgtgctgcag	gctgcacggg	tcccaagcat	tctgactgcc	tggcctgcct	ccacttcaat	780
catagtggta	tctgtgagct	gcactgcccg	gccctcatca	cctacaacac	agacaccttc	840
gagtccatgc	tcaacctga	gggtcgctac	acctttgggtg	ccagctgtgt	gaccacctgc	900
ccctacaact	acctctccac	ggaagtggga	tctgcactc	tggctctgtcc	cccgaacaac	960
caagaggtca	cagctgagga	cggaaacacag	cgggtgtgaga	aatgcagcaa	gccctgtgct	1020
ggagtatgct	atggtctggg	catggagcac	ctccgagggg	cgaggggccat	caccagtgc	1080
aatatccagg	agtttgctgg	ctgcaagaag	atctttggga	gcctggcatt	tttgccggag	1140
agctttgatg	ggaacccctc	ctccggcggt	gccccactga	agccagagca	tctccaagtg	1200
ttcgaacccc	tggaggagat	cacaggttac	ctatacattt	cagcatggcc	agagagcttc	1260
caagacctca	gtgtcttcca	gaaccttcgg	gtcattcggg	gacggattct	ccatgatggt	1320
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gagctgggca	gtggattggc	tctcattcac	cgcaacaccc	atctctgctt	tgtaaacact	1440
gtaccttggg	accagctctt	ccggaacccg	caccaggccc	tactccacag	tgggaaccgg	1500
ccagaagagg	catgtggtct	tgagggtctg	gtctgttaact	cactgtgtgc	ccgtgggcac	1560
tgtgtggggc	cagggcccac	ccagtgtgtc	aactgcagtc	agttcctccg	ggggccaggag	1620
tgtgtggagg	agtgccgagt	atggaagggg	ctccccaggg	agtatgtgag	gggcaagcac	1680
tgtctgccat	gccaccccga	gtgtcagcct	caaaacagct	cggagacctg	ctatggatcg	1740
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gagggcatat	gtcagccatg	ccccatcaac	tgcacccact	catgtgtgga	cctggacgaa	1920
cgaggctgcc	cagcagagca	gagagccagc	ccagtgcacat	tcatcattgc	aactgtgggtg	1980
ggcgtcctgt	tgttctctgat	catagtgggtg	gtcattggaa	tcctaataca	acgaaggcga	2040
cagaagatcc	ggaagtatac	catgcgtagg	ctgctgcagg	agaccgagct	ggtggagccg	2100
ctgacgccc	gtggagctgt	gcccacaccag	gctcagatgc	ggatcctaaa	ggagacagag	2160
ctaaggaagc	tgaaggtgct	tgggtcagga	gccttcggca	ctgtctacaa	gggcatctgg	2220
atcccagatg	gggagaacgt	gaaaatcccc	gtggccatca	aggtgttgag	ggaaaacaca	2280
tctcctaaag	ctaacaaga	aatcctagat	gaagcgtacg	tcatggctgg	tgtgggtctct	2340
ccatatgtgt	cccgcctcct	gggcatctgc	ctgacatcca	cagtgcagct	ggtgcacacag	2400
cttatgccct	atggctgcct	tctggaccat	gtccgagaac	accgaggtcg	cttaggctcc	2460
caggacctgc	tcaactgggtg	tgttcagatt	gccaagggga	tgagctacct	ggaggaagtt	2520
cggcttgctc	acagggacct	agctgcccga	aacgtgctag	tcaagagtcc	caaccacgtc	2580
aagattaccg	acttcgggct	ggcacggctg	ctggacattg	atgagactga	ataccatgca	2640
gatgggggca	aggtgcccac	caagtggatg	gcattggaat	ctattctcag	acgccgggtc	2700
actcatcaga	gtgatgtgtg	gagctatggt	gtgactgtgt	gggagctgat	gacctttggg	2760
gccaaacctt	acgatgggat	cccagctcgg	gagatccctg	atttgctgga	gaaggagaa	2820
cgcctacctc	agcctccaat	ctgcaccatc	gacgtctaca	tgatcatggt	caaatggttg	2880
atgattgact	ccgaatgtcg	cccgagattc	cgggagttgg	tatcagaatt	ctcccgtatg	2940
gcaagggacc	cccagcgctt	tgtggctcct	cagaacgagg	acttaggccc	ctccagcccc	3000
atggacagca	ccttctaccg	tctactgctg	gaggatgatg	acatggggga	gctggctgat	3060
gctgaagagt	acctggtacc	ccagcaggga	ttcttctccc	cagaccctgc	cctagggtact	3120
gggagcacag	cccaccgcag	acaccgcagc	tctgtcggcca	ggagtggcgg	tgggtgagctg	3180
acactggggc	tggagccctc	ggaagaagag	ccccccagat	ctccactggc	tccctccgaa	3240
ggggctggct	ccgatgtgtt	tgatggtgac	ctggcagtg	gggtaaccaa	aggactgcag	3300
agcctctctc	cacatgacct	cagccctcta	cagcggatca	gtgaggatcc	cacattacct	3360

[illegible]

Met	Glu	Leu	Ala	Ala	Ala	Trp	Cys	Arg	Trp	Gly	Phe	Leu	Leu	Ala	Leu	Leu
1					5					10					15	
Ser	Pro	Gly	Ala	Ala	Gly	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys	
			20					25					30			
Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	Leu	Arg	His	
		35					40					45				
Leu	Tyr	Gln	Gly	Cys	Gln	Val	Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr		
	50					55				60						
Leu	Pro	Ala	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val	
65					70					75					80	
Gln	Gly	Tyr	Met	Leu	Ile	Ala	His	Asn	Arg	Val	Lys	His	Val	Pro	Leu	
				85					90					95		
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Lys	Tyr	
			100					105						110		
Ala	Leu	Ala	Val	Leu	Asp	Asn	Arg	Asp	Pro	Leu	Asp	Asn	Val	Thr	Thr	
		115					120					125				
Ala	Ala	Pro	Gly	Arg	Thr	Pro	Glu	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	
	130					135					140					
Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Arg	Gly	Asn	Pro	
145					150					155					160	
Gln	Leu	Cys	Tyr	Gln	Asp	Met	Val	Leu	Trp	Lys	Asp	Val	Leu	Arg	Lys	
				165					170					175		
Asn	Asn	Gln	Leu	Ala	Pro	Val	Asp	Met	Asp	Thr	Asn	Arg	Ser	Arg	Ala	
			180					185					190			
Cys	Pro	Pro	Cys	Ala	Pro	Thr	Cys	Lys	Asp	Asn	His	Cys	Trp	Gly	Glu	
		195					200					205				
Ser	Pro	Glu	Asp	Cys	Gln	Ile	Leu	Thr	Gly	Thr	Ile	Cys	Thr	Ser	Gly	
	210					215					220					
Cys	Ala	Arg	Cys	Lys	Gly	Arg	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	
225					230					235					240	
Cys	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	
				245					250					255		
Leu	His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	
			260					265					270			
Ile	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Leu	Asn	Pro	Glu	Gly	
		275					280						285			
Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Thr	Cys	Pro	Tyr	Asn	Tyr	
	290					295					300					
Leu	Ser	Thr	Glu	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Pro	Asn	Asn	
305					310					315					320	
Gln	Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	
				325					330					335		
Lys	Pro	Cys	Ala	Gly	Val	Cys										

Fig. 20 (SEQ ID NO:14)

			420					425					430				
Arg	Gly	Arg	Ile	Leu	His	Asp	Gly	Ala	Tyr	Ser	Leu	Thr	Leu	Gln	Gly		
		435					440						445				
Leu	Gly	Ile	His	Ser	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	Leu	Gly	Ser		
	450					455					460						
Gly	Leu	Ala	Leu	Ile	His	Arg	Asn	Thr	His	Leu	Cys	Phe	Val	Asn	Thr		
465					470					475					480		
Val	Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His		
			485						490					495			
Ser	Gly	Asn	Arg	Pro	Glu	Glu	Ala	Cys	Gly	Leu	Glu	Gly	Leu	Val	Cys		
		500						505					510				
Asn	Ser	Leu	Cys	Ala	Arg	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln		
	515						520					525					
Cys	Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	Val	Glu	Glu		
	530					535					540						
Cys	Arg	Val	Trp	Lys	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Arg	Gly	Lys	His		
545					550					555					560		
Cys	Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Ser	Ser	Glu	Thr		
			565						570					575			
Cys	Tyr	Gly	Ser	Glu	Ala	Asp	Gln	Cys	Glu	Ala	Cys	Ala	His	Tyr	Lys		
			580					585					590				
Asp	Ser	Ser	Ser	Cys	Val	Ala	Arg	Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp		
	595						600					605					
Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	Tyr	Pro	Asp	Glu	Glu	Gly	Ile	Cys		
	610					615					620						
Gln	Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Glu		
625					630					635					640		
Arg	Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Val	Thr	Phe	Ile	Ile		
			645						650					655			
Ala	Thr	Val	Val	Gly	Val	Leu	Leu	Phe	Leu	Ile	Ile	Val	Val	Val	Ile		
			660					665					670				
Gly	Ile	Leu	Ile	Lys	Arg	Arg	Arg	Gln	Lys	Ile	Arg	Lys	Tyr	Thr	Met		
	675						680					685					
Arg	Arg	Leu	Leu	Gln	Glu	Thr	Glu	Leu	Val	Glu	Pro	Leu	Thr	Pro	Ser		
	690					695					700						
Gly	Ala	Val	Pro	Asn	Gln	Ala	Gln	Met	Arg	Ile	Leu	Lys	Glu	Thr	Glu		
705					710					715					720		
Leu	Arg	Lys	Leu	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr		
			725						730					735			
Lys	Gly	Ile	Trp	Ile	Pro	Asp	Gly	Glu	Asn	Val	Lys	Ile	Pro	Val	Ala		
			740					745					750				
Ile	Lys	Val	Leu	Arg	Glu	Asn	Thr	Ser	Pro	Lys	Ala	Asn	Lys	Glu	Ile		
	755					760						765					
Leu	Asp	Glu	Ala	Tyr	Val	Met	Ala	Gly	Val	Gly	Ser	Pro	Tyr	Val	Ser		
	770					775					780						
Arg	Leu	Leu	Gly	Ile	Cys	Leu	Thr	Ser	Thr	Val	Gln	Leu	Val	Thr	Gln		
785					790					795					800		
Leu	Met	Pro	Tyr	Gly	Cys	Leu	Leu	Asp	His	Val	Arg	Glu	His	Arg	Gly		
			805						810					815			
Arg	Leu	Gly	Ser	Gln	Asp	Leu	Leu	Asn	Trp	Cys	Val	Gln	Ile	Ala	Lys		
			820					825					830				
Gly	Met	Ser	Tyr	Leu	Glu	Glu	Val	Arg	Leu	Val	His	Arg	Asp	Leu	Ala		
	835						840					845					
Ala	Arg	Asn	Val	Leu	Val	Lys	Ser	Pro	Asn	His	Val	Lys	Ile	Thr	Asp		
	850					855					860						
Phe	Gly	Leu	Ala	Arg	Leu	Leu	Asp	Ile	Asp	Glu	Thr	Glu	Tyr	His	Ala		
865					870					875					880		

Fig. 20 (SEQ ID NO:14)

Asp Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu
 885 890 895
 Arg Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr
 900 905 910
 Val Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro
 915 920 925
 Ala Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln
 930 935 940
 Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp
 945 950 955 960
 Met Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu
 965 970 975
 Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn
 980 985 990
 Glu Asp Leu Gly Pro Ser Ser Pro Met Asp Ser Thr Phe Tyr Arg Ser
 995 1000 1005
 Leu Leu Glu Asp Asp Asp Met Gly Glu Leu Val Asp Ala Glu Glu Tyr
 1010 1015 1020
 Leu Val Pro Gln Gln Gly Phe Phe Ser Pro Asp Pro Ala Leu Gly Thr
 1025 1030 1035 1040
 Gly Ser Thr Ala His Arg Arg His Arg Ser Ser Ser Ala Arg Ser Gly
 1045 1050 1055
 Gly Gly Glu Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Pro Pro
 1060 1065 1070
 Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp
 1075 1080 1085
 Gly Asp Leu Ala Val Gly Val Thr Lys Gly Leu Gln Ser Leu Ser Pro
 1090 1095 1100
 His Asp Leu Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Leu Pro
 1105 1110 1115 1120
 Leu Pro Pro Glu Thr Asp Gly Tyr Val Ala Pro Leu Ala Cys Ser Pro
 1125 1130 1135
 Gln Pro Glu Tyr Val Asn Gln Pro Glu Val Arg Pro Gln Ser Pro Leu
 1140 1145 1150
 Thr Pro Glu Gly Pro Pro Pro Pro Ile Arg Pro Ala Gly Ala Thr Leu
 1155 1160 1165
 Glu Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp
 1170 1175 1180
 Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Ala Pro
 1185 1190 1195 1200
 Arg Ala Gly Thr Ala Ser Gln Pro His Pro Ser Pro Ala Phe Ser Pro
 1205 1210 1215
 Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asn Ser Ser Glu Gln Gly
 1220 1225 1230
 Pro Pro Pro Ser Thr Phe Glu Gly Thr Pro Thr Ala Glu Asn Pro Glu
 1235 1240 1245
 Tyr Leu Gly Leu Asp Val Pro Val
 1250 1255

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